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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/942,087A

DATE: 05/09/2002
TIME: 13:00:36

Input Set : A:\seqlist.txt
Output Set: N:\CRF3\05092002\I942087A.raw

3 <110> APPLICANT: Case, Casey Christopher
4 Wolffe, Alan
5 Urnov, Fyodor
6 Lai, Albert
7 Snowden, Andrew
8 Tan, Siyuan
9 Gregory, Philip
11 <120> TITLE OF INVENTION: MODULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS
13 <130> FILE REFERENCE: 8325-0002.21 / S2-US5
15 <140> CURRENT APPLICATION NUMBER: 09/942,087A
16 <141> CURRENT FILING DATE: 2001-08-28
18 <150> PRIOR APPLICATION NUMBER: 09/229,037
19 <151> PRIOR FILING DATE: 1999-01-12
21 <160> NUMBER OF SEQ ID NOS: 43
23 <170> SOFTWARE: PatentIn Ver. 2.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 25
27 <212> TYPE: PRT
28 <213> ORGANISM: Artificial Sequence
30 <220> FEATURE:
31 <223> OTHER INFORMATION: Description of Artificial Sequence:exemplary motif
32 of C2H2 class of zinc finger proteins (ZFP)
34 <220> FEATURE:
35 <221> NAME/KEY: MOD_RES
36 <222> LOCATION: (2)..(3)
37 <223> OTHER INFORMATION: Xaa = any amino acid
39 <220> FEATURE:
40 <221> NAME/KEY: MOD_RES
41 <222> LOCATION: (4)..(5)
42 <223> OTHER INFORMATION: Xaa = any amino acid, may be present or absent
44 <220> FEATURE:
45 <221> NAME/KEY: MOD_RES
46 <222> LOCATION: (7)..(18)
47 <223> OTHER INFORMATION: Xaa = any amino acid
49 <220> FEATURE:
50 <221> NAME/KEY: MOD_RES
51 <222> LOCATION: (20)..(22)
52 <223> OTHER INFORMATION: Xaa = any amino acid
54 <220> FEATURE:
55 <221> NAME/KEY: MOD_RES
56 <222> LOCATION: (23)..(24)
57 <223> OTHER INFORMATION: Xaa = any amino acid, may be present or absent
59 <400> SEQUENCE: 1

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W--> 60 Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
61      1              5              10              15
W--> 63 Xaa Xaa His Xaa Xaa Xaa Xaa Xaa His
64      20              25
65 <210> SEQ ID NO: 2
66 <211> LENGTH: 10
67 <212> TYPE: DNA
68 <213> ORGANISM: Artificial Sequence
69 <220> FEATURE:
70 <223> OTHER INFORMATION: Description of Artificial Sequence:ZFP target site
71      with two overlapping D-able subsites
72 <220> FEATURE:
73 <221> NAME/KEY: modified_base
74 <222> LOCATION: (1)..(2)
75 <223> OTHER INFORMATION: n = g,a,c or t
76 <220> FEATURE:
77 <221> NAME/KEY: modified_base
78 <222> LOCATION: (5)
79 <223> OTHER INFORMATION: n = g,a,c or t
80 <220> FEATURE:
81 <221> NAME/KEY: modified_base
82 <222> LOCATION: (8)
83 <223> OTHER INFORMATION: n = g,a,c or t
84 <220> FEATURE:
85 <221> NAME/KEY: modified_base
86 <222> LOCATION: (9)
87 <223> OTHER INFORMATION: n = a,c or t; if g, then position 10 cannot be g
88      or t
89 <220> FEATURE:
90 <221> NAME/KEY: modified_base
91 <222> LOCATION: (10)
92 <223> OTHER INFORMATION: n = a or c; if g or t, then position 9 cannot be g
93 <400> SEQUENCE: 2
W--> 101 nngkngknnn
104      10
104 <210> SEQ ID NO: 3
105 <211> LENGTH: 10
106 <212> TYPE: DNA
107 <213> ORGANISM: Artificial Sequence
108 <220> FEATURE:
109 <223> OTHER INFORMATION: Description of Artificial Sequence:ZFP target site
110      with three overlapping D-able subsites
111 <220> FEATURE:
112 <221> NAME/KEY: modified_base
113 <222> LOCATION: (1)..(2)
114 <223> OTHER INFORMATION: n = g,a,c or t
115 <220> FEATURE:
116 <221> NAME/KEY: modified_base
117 <222> LOCATION: (5)
118 <223> OTHER INFORMATION: n = g,a,c or t

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124 <220> FEATURE:
125 <221> NAME/KEY: modified_base
126 <222> LOCATION: (8)
127 <223> OTHER INFORMATION: n = g,a,c or t
129 <400> SEQUENCE: 3
W--> 130 nngkngkngk 10
133 <210> SEQ ID NO: 4
134 <211> LENGTH: 5
135 <212> TYPE: PRT
136 <213> ORGANISM: Artificial Sequence
138 <220> FEATURE:
139 <223> OTHER INFORMATION: Description of Artificial Sequence:linker
141 <400> SEQUENCE: 4
142 Asp Gly Gly Gly Ser
143 1 5
146 <210> SEQ ID NO: 5
147 <211> LENGTH: 5
148 <212> TYPE: PRT
149 <213> ORGANISM: Artificial Sequence
151 <220> FEATURE:
152 <223> OTHER INFORMATION: Description of Artificial Sequence:linker
154 <400> SEQUENCE: 5
155 Thr Gly Glu Lys Pro
156 1 5
159 <210> SEQ ID NO: 6
160 <211> LENGTH: 9
161 <212> TYPE: PRT
162 <213> ORGANISM: Artificial Sequence
164 <220> FEATURE:
165 <223> OTHER INFORMATION: Description of Artificial Sequence:linker
167 <400> SEQUENCE: 6
168 Leu Arg Gln Lys Asp Gly Glu Arg Pro
169 1 5
172 <210> SEQ ID NO: 7
173 <211> LENGTH: 4
174 <212> TYPE: PRT
175 <213> ORGANISM: Artificial Sequence
177 <220> FEATURE:
178 <223> OTHER INFORMATION: Description of Artificial Sequence:linker
180 <400> SEQUENCE: 7
181 Gly Gly Arg Arg
182 1
185 <210> SEQ ID NO: 8
186 <211> LENGTH: 5
187 <212> TYPE: PRT
188 <213> ORGANISM: Artificial Sequence
190 <220> FEATURE:
191 <223> OTHER INFORMATION: Description of Artificial Sequence:linker
193 <400> SEQUENCE: 8

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194 Gly Gly Gly Gly Ser
195   1           5
198 <210> SEQ ID NO: 9
199 <211> LENGTH: 8
200 <212> TYPE: PRT
201 <213> ORGANISM: Artificial Sequence
203 <220> FEATURE:
204 <223> OTHER INFORMATION: Description of Artificial Sequence:linker
206 <400> SEQUENCE: 9
207 Gly Gly Arg Arg Gly Gly Ser
208   1           5
211 <210> SEQ ID NO: 10
212 <211> LENGTH: 9
213 <212> TYPE: PRT
214 <213> ORGANISM: Artificial Sequence
216 <220> FEATURE:
217 <223> OTHER INFORMATION: Description of Artificial Sequence:linker
219 <400> SEQUENCE: 10
220 Leu Arg Gln Arg Asp Gly Glu Arg Pro
221   1           5
224 <210> SEQ ID NO: 11
225 <211> LENGTH: 12
226 <212> TYPE: PRT
227 <213> ORGANISM: Artificial Sequence
229 <220> FEATURE:
230 <223> OTHER INFORMATION: Description of Artificial Sequence:linker
232 <400> SEQUENCE: 11
233 Leu Arg Gln Lys Asp Gly Gly Gly Ser Glu Arg Pro
234   1           5           10
237 <210> SEQ ID NO: 12
238 <211> LENGTH: 16
239 <212> TYPE: PRT
240 <213> ORGANISM: Artificial Sequence
242 <220> FEATURE:
243 <223> OTHER INFORMATION: Description of Artificial Sequence:linker
246 <400> SEQUENCE: 12
247 Leu Arg Gln Lys Asp Gly Gly Gly Ser Gly Gly Gly Ser Glu Arg Pro
248   1           5           10           15
251 <210> SEQ ID NO: 13
252 <211> LENGTH: 25
253 <212> TYPE: DNA
254 <213> ORGANISM: Artificial Sequence
256 <220> FEATURE:
257 <223> OTHER INFORMATION: Description of Artificial Sequence:ZFP target site
258     region surrounding initiation site of vascular
259     endothelial growth factor (VEGF) gene containing
260     two 9-base pair target sites
262 <220> FEATURE:
263 <221> NAME/KEY: protein_bind

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```

264 <222> LOCATION: (4)..(12)
265 <223> OTHER INFORMATION: upstream 9-base pair ZFP VEGF1 target site
267 <220> FEATURE:
268 <221> NAME/KEY: protein_bind
269 <222> LOCATION: (14)..(22)
270 <223> OTHER INFORMATION: downstream 9-base pair ZFP VEGF3a target site
272 <400> SEQUENCE: 13
273 agcggggagg atcgcgagg cttgg 25
276 <210> SEQ ID NO: 14
277 <211> LENGTH: 298
278 <212> TYPE: DNA
279 <213> ORGANISM: Artificial Sequence
281 <220> FEATURE:
282 <223> OTHER INFORMATION: Description of Artificial Sequence:VEGF1 ZFP
283     construct targeting upstream 9-base pair target
284     site in VEGF promoter
286 <220> FEATURE:
287 <221> NAME/KEY: CDS
288 <222> LOCATION: (2)..(298)
289 <223> OTHER INFORMATION: VEGF1
291 <400> SEQUENCE: 14
292 g gta ccc ata cct ggc aag aag aag cag cac atc tgc cac atc cag ggc 49
293   Val Pro Ile Pro Gly Lys Lys Lys Gln His Ile Cys His Ile Gln Gly
294     1           5           10           15
296 tgt ggt aaa gtt tac ggc aca acc tca aat ctg cgt cgt cac ctg cgc 97
297 Cys Gly Lys Val Tyr Gly Thr Thr Ser Asn Leu Arg Arg His Leu Arg
298           20           25           30
300 tgg cac acc ggc gag agg cct ttc atg tgt acc tgg tcc tac tgt ggt 145
301 Trp His Thr Gly Glu Arg Pro Phe Met Cys Thr Trp Ser Tyr Cys Gly
302           35           40           45
304 aaa cgc ttc acc cgt tcg tca aac ctg cag cgt cac aag cgt acc cac 193
305 Lys Arg Phe Thr Arg Ser Ser Asn Leu Gln Arg His Lys Arg Thr His
306           50           55           60
307 acc ggt gag aag aaa ttt gct tgc ccg gag tgt ccg aag cgc ttc atg 241
308 Thr Gly Glu Lys Lys Phe Ala Cys Pro Glu Cys Pro Lys Arg Phe Met
309           65           70           75           80
311 cgt agt gac cac ctg tcc cgt cac atc aag acc cac cag aat aag aag 289
312 Arg Ser Asp His Leu Ser Arg His Ile Lys Thr His Gln Asn Lys Lys
313           85           90           95
315 ggt gga tcc 298
316 Gly Gly Ser
319 <210> SEQ ID NO: 15
320 <211> LENGTH: 99
321 <212> TYPE: PRT
322 <213> ORGANISM: Artificial Sequence
324 <220> FEATURE:
325 <223> OTHER INFORMATION: Description of Artificial Sequence:VEGF1 ZFP
326     construct targeting upstream 9-base pair target
327     site in VEGF promoter

```

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 05/09/2002
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 2,3,4,5,7,8,9,10,11,12,13,14,15,16,17,18,20,21,22,23,24
Seq#:2; N Pos. 1,2,5,8,9,10
Seq#:3; N Pos. 1,2,5,8
Seq#:41; N Pos. 1,2
Seq#:42; N Pos. 1,2
Seq#:43; N Pos. 1,2

VARIABLE LOCATION SUMMARY DATE: 05/09/2002
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Use of n's or Xaa's (NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:1; Xaa Pos. 2,3,4,5,7,8,9,10,11,12,13,14,15,16,17,18,20,21,22,23,24

Seq#:2; N Pos. 1,2,5,8,9,10

Seq#:3; N Pos. 1,2,5,8

Seq#:41; N Pos. 1,2

Seq#:42; N Pos. 1,2

Seq#:43; N Pos. 1,2

VERIFICATION SUMMARY

DATE: 05/09/2002

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Input Set : A:\seqlist.txt

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L:60 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:63 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:16
L:101 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
L:130 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:865 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:41
L:865 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:41
L:865 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41 after pos.:0
L:877 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:42
L:877 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:42
L:877 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42 after pos.:0
L:889 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:43
L:889 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:43
L:889 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43 after pos.:0